

GG GCG CGA GCG CCT CAG CGC GGC CGC TCG CTC TCC CCC 38
 Ala Arg Ala Pro Gln Arg Gly Arg Ser Leu Ser Pro
 1 5 10

TCG AGG GAC AAA CTT TTC CCA AAC CCG ATC CGA GCC CTT 77
 Ser Arg Asp Lys Leu Phe Pro Asn Pro Ile Arg Ala Leu
 15 20 25

GGA CCA AAC TCG CCT GCG CCG AGA GCC GTC CGC GTA GAG 116
 Gly Pro Asn Ser Pro Ala Pro Arg Ala Val Arg Val Glu
 30 35

CGC TCC GTC TCC GGC GAG ATG TCC GAG CGC AAA GAA GGC 155
 Arg Ser Val Ser Gly Glu Met Ser Glu Arg Lys Glu Gly
 40 45 50

AGA GGC AAA GGG AAG GGC AAG AAG AAG GAG CGA GGC TCC 194
 Arg Gly Lys Gly Lys Gly Lys Lys Glu Arg Gly Ser
 55 60

GGC AAG AAG CCG GAG TCC GCG GCG GGC AGC CAG AGC CCA 233
 Gly Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser Pro
 65 70 75

GCC TTG CCT CCC CGA TTG AAA GAG ATG AAA AGC CAG GAA 272
 Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu
 80 85 90

TCG GCT GCA GGT TCC AAA CTA GTC CTT CGG TGT GAA ACC 311
 Ser Ala Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr
 95 100

AGT TCT GAA TAC TCC TCT CTC AGA TTC AAG TGG TTC AAG 350
 Ser Ser Glu Tyr Ser Ser Leu Arg Phe Lys Trp Phe Lys
 105 110 115

AAT GGG AAT GAA TTG AAT CGA AAA AAC AAA CCA CAA AAT 389
 Asn Gly Asn Glu Leu Asn Arg Lys Asn Lys Pro Gln Asn
 120 125

ATC AAG ATA CAA AAA AAG CCA GGG AAG TCA GAA CTT CGC 428
 Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu Leu Arg
 130 135 140

ATT AAC AAA GCA TCA CTG GCT GAT TCT GGA GAG TAT ATG 467
 Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met
 145 150 155

TGC AAA GTG ATC AGC AAA TTA GGA AAT GAC AGT GCC TCT 506
 Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser
 160 165

GCC AAT ATC ACC ATC GTG GAA TCA AAC GAG ATC ATC ACT 545
 Ala Asn Ile Thr Ile Val Glu Ser Asn Glu Ile Ile Thr
 170 175 180

 GGT ATG CCA GCC TCA ACT GAA GGA GCA TAT GTG TCT TCA 584
 Gly Met Pro Ala Ser Thr Glu Gly Ala Tyr Val Ser Ser
 185 190

 GAG TCT CCC ATT AGA ATA TCA GTA TCC ACA GAA GGA GCA 623
 Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Ala
 195 200 205

 AAT ACT TCT TCA TCT ACA TCT ACA TCC ACC ACT GGG ACA 662
 Asn Thr Ser Ser Ser Thr Ser Thr Thr Gly Thr
 210 215 220

 AGC CAT CTT GTA AAA TGT GCG GAG AAG GAG AAA ACT TTC 701
 Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe
 225 230

 TGT GTG AAT GGA GGG GAG TGC TTC ATG GTG AAA GAC CTT 740
 Cys Val Asn Gly Gly Glu Cys Phe Met Val Lys Asp Leu
 235 240 245

 TCA AAC CCC TCG AGA TAC TTG TGC AAG TGC CAA CCT GGA 779
 Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys Gln Pro Gly
 250 255

 TTC ACT GGA GCA AGA TGT ACT GAG AAT GTG CCC ATG AAA 818
 Phe Thr Gly Ala Arg Cys Thr Glu Asn Val Pro Met Lys
 260 265 270

 GTC CAA AAC CAA GAA AAG GCG GAG GAG CTG TAC CAG AAG 857
 Val Gln Asn Gln Glu Lys Ala Glu Glu Leu Tyr Gln Lys
 275 280 285

 AGA GTG CTG ACC ATA ACC GGC ATC TGC ATC GCC CTC CTT 896
 Arg Val Leu Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu
 290 295

 GTG GTC GGC ATC ATG TGT GTG GTG GCC TAC TGC AAA ACC 935
 Val Val Gly Ile Met Cys Val Val Ala Tyr Cys Lys Thr
 300 305 310

 AAG AAA CAG CGG AAA AAG CTG CAT GAC CGT CTT CGG CAG 974
 Lys Lys Gln Arg Lys Lys Leu His Asp Arg Leu Arg Gln
 315 320

 AGC CTT CGG TCT GAA CGA AAC AAT ATG ATG AAC ATT GCC 1013
 Ser Leu Arg Ser Glu Arg Asn Asn Met Met Asn Ile Ala
 325 330 335

FIG. 1B

AAT GGG CCT CAC CAT CCT AAC CCA CCC CCC GAG AAT GTC 1052
 Asn Gly Pro His His Pro Asn Pro Pro Pro Glu Asn Val
 340 345 350

CAG CTG GTG AAT CAA TAC GTA TCT AAA AAC GTC ATC TCC 1091
 Gln Leu Val Asn Gln Tyr Val Ser Lys Asn Val Ile Ser
 355 360

AGT GAG CAT ATT GTT GAG AGA GAA GCA GAG ACA TCC TTT 1130
 Ser Glu His Ile Val Glu Arg Glu Ala Glu Thr Ser Phe
 365 370 375

TCC ACC AGT CAC TAT ACT TCC ACA GCC CAT CAC TCC ACT 1169
 Ser Thr Ser His Tyr Thr Ser Thr Ala His His Ser Thr
 380 385

ACT GTC ACC CAG ACT CCT AGC CAC AGC TGG AGC AAC GGA 1208
 Thr Val Thr Gln Thr Pro Ser His Ser Trp Ser Asn Gly
 390 395 400

CAC ACT GAA AGC ATC CTT TCC GAA AGC CAC TCT GTA ATC 1247
 His Thr Glu Ser Ile Leu Ser Glu Ser His Ser Val Ile
 405 410 415

GTG ATG TCA TCC GTA GAA AAC AGT AGG CAC AGC AGC CCA 1286
 Val Met Ser Ser Val Glu Asn Ser Arg His Ser Ser Pro
 420 425

ACT GGG GGC CCA AGA GGA CGT CTT AAT GGC ACA GGA GGC 1325
 Thr Gly Gly Pro Arg Gly Arg Leu Asn Gly Thr Gly Gly
 430 435 440

CCT CGT GAA TGT AAC AGC TTC CTC AGG CAT GCC AGA GAA 1364
 Pro Arg Glu Cys Asn Ser Phe Leu Arg His Ala Arg Glu
 445 450

ACC CCT GAT TCC TAC CGA GAC TCT CCT CAT AGT GAA AGG 1403
 Thr Pro Asp Ser Tyr Arg Asp Ser Pro His Ser Glu Arg
 455 460 465

TAT GTG TCA GCC ATG ACC ACC CCG GCT CGT ATG TCA CCT 1442
 Tyr Val Ser Ala Met Thr Thr Pro Ala Arg Met Ser Pro
 470 475 480

GTA GAT TTC CAC ACG CCA AGC TCC CCC AAA TCG CCC CCT 1481
 Val Asp Phe His Thr Pro Ser Ser Pro Lys Ser Pro Pro
 485 490

TCG GAA ATG TCT CCA CCC GTG TCC AGC ATG ACG GTG TCC 1520
 Ser Glu Met Ser Pro Pro Val Ser Ser Met Thr Val Ser
 495 500 505

FIG. 1C

ATG CCT TCC ATG GCG GTC AGC CCC TTC ATG GAA GAA GAG 1559
 Met Pro Ser Met Ala Val Ser Pro Phe Met Glu Glu Glu
 510 515

AGA CCT CTA CTT CTC GTG ACA CCA CCA AGG CTG CGG GAG 1598
 Arg Pro Leu Leu Leu Val Thr Pro Pro Arg Leu Arg Glu
 520 525 530

AAG AAG TTT GAC CAT CAC CCT CAG CAG TTC AGC TCC TTC 1637
 Lys Lys Phe Asp His His Pro Gln Gln Phe Ser Ser Phe
 535 540 545

CAC CAC AAC CCC GCG CAT GAC AGT AAC AGC CTC CCT GCT 1676
 His His Asn Pro Ala His Asp Ser Asn Ser Leu Pro Ala
 550 555

AGC CCC TTG AGG ATA GTG GAG GAT GAG GAG TAT GAA ACG 1715
 Ser Pro Leu Arg Ile Val Glu Asp Glu Glu Tyr Glu Thr
 560 565 570

ACC CAA GAG TAC GAG CCA GCC CAA GAG CCT GTT AAG AAA 1754
 Thr Gln Glu Tyr Glu Pro Ala Gln Glu Pro Val Lys Lys
 575 580

CTC GCC AAT AGC CGG CGG GCC AAA AGA ACC AAG CCC AAT 1793
 Leu Ala Asn Ser Arg Arg Ala Lys Arg Thr Lys Pro Asn
 585 590 595

GGC CAC ATT GCT AAC AGA TTG GAA GTG GAC AGC AAC ACA 1832
 Gly His Ile Ala Asn Arg Leu Glu Val Asp Ser Asn Thr
 600 605 610

AGC TCC CAG AGC AGT AAC TCA GAG AGT GAA ACA GAA GAT 1871
 Ser Ser Gln Ser Ser Asn Ser Glu Ser Glu Thr Glu Asp
 615 620

GAA AGA GTA GGT GAA GAT ACG CCT TTC CTG GGC ATA CAG 1910
 Glu Arg Val Gly Glu Asp Thr Pro Phe Leu Gly Ile Gln
 625 630 635

AAC CCC CTG GCA GCC AGT CTT GAG GCA ACA CCT GCC TTC 1949
 Asn Pro Leu Ala Ala Ser Leu Glu Ala Thr Pro Ala Phe
 640 645

CGC CTG GCT GAC AGC AGG ACT AAC CCA GCA GGC CGC TTC 1988
 Arg Leu Ala Asp Ser Arg Thr Asn Pro Ala Gly Arg Phe
 650 655 660

TCG ACA CAG GAA GAA ATC CAG G 2010
 Ser Thr Gln Glu Glu Ile Gln
 665 669

FIG. 1D

GG GAC AAA CTT TTC CCA AAC CCG ATC CGA GCC CTT GGA 38
 Asp Lys Leu Phe Pro Asn Pro Ile Arg Ala Leu Gly
 1 5 10

CCA AAC TCG CCT GCG CCG AGA GCC GTC CGC GTA GAG CGC 77
 Pro Asn Ser Pro Ala Pro Arg Ala Val Arg Val Glu Arg
 15 20 25

TCC GTC TCC GGC GAG ATG TCC GAG CGC AAA GAA GGC AGA 116
 Ser Val Ser Gly Glu Met Ser Glu Arg Lys Glu Gly Arg
 30 35

GGC AAA GGG AAG GGC AAG AAG GAG CGA GGC TCC GGC 155
 Gly Lys Gly Lys Gly Lys Lys Glu Arg Gly Ser Gly
 40 45 50

AAG AAG CCG GAG TCC GCG GCG AGC CAG AGC CCA GCC 194
 Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser Pro Ala
 55 60

TTG CCT CCC CAA TTG AAA GAG ATG AAA AGC CAG GAA TCG 233
 Leu Pro Pro Gln Leu Lys Glu Met Lys Ser Gln Glu Ser
 65 70 75

GCT GCA GGT TCC AAA CTA GTC CTT CGG TGT GAA ACC AGT 272
 Ala Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser
 80 85 90

TCT GAA TAC TCC TCT CTC AGA TTC AAG TGG TTC AAG AAT 311
 Ser Glu Tyr Ser Ser Leu Arg Phe Lys Trp Phe Lys Asn
 95 100

GGG AAT GAA TTG AAT CGA AAA AAC AAA CCA CAA AAT ATC 350
 Gly Asn Glu Leu Asn Arg Lys Asn Lys Pro Gln Asn Ile
 105 110 115

AAG ATA CAA AAA AAG CCA GGG AAG TCA GAA CTT CGC ATT 389
 Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu Leu Arg Ile
 120 125

AAC AAA GCA TCA CTG GCT GAT TCT GGA GAG TAT ATG TGC 428
 Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys
 130 135 140

AAA GTG ATC AGC AAA TTA GGA AAT GAC AGT GCC TCT GCC 467
 Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala
 145 150 155

AAT ATC ACC ATC GTG GAA TCA AAC GAG ATC ATC ACT GGT 506
 Asn Ile Thr Ile Val Glu Ser Asn Glu Ile Ile Thr Gly
 160 165

FIG.2A

ATG CCA GCC TCA ACT GAA GGA GCA TAT GTG TCT TCA GAG 545
 Met Pro Ala Ser Thr Glu Gly Ala Tyr Val Ser Ser Glu
 170 175 180

 TCT CCC ATT AGA ATA TCA GTA TCC ACA GAA GGA GCA AAT 584
 Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Ala Asn
 185 190

 ACT TCT TCA TCT ACA TCT ACA TCC ACC ACT GGG ACA AGC 623
 Thr Ser Ser Thr Ser Thr Thr Gly Thr Ser
 195 200 205

 CAT CTT GTA AAA TGT GCG GAG AAG GAG AAA ACT TTC TGT 662
 His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys
 210 215 220

 GTG AAT GGA GGG GAG TGC TTC ATG GTG AAA GAC CTT TCA 701
 Val Asn Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser
 225 230

 AAC CCC TCG AGA TAC TTG TGC AAG TGC CCA AAT GAG TTT 740
 Asn Pro Ser Arg Tyr Leu Cys Lys Cys Pro Asn Glu Phe
 235 240 245

 ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC 779
 Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe
 250 255

 TAC AAG CAT CTT GGG ATT GAA TTT ATG GAG GCG GAG GAG 818
 Tyr Lys His Leu Gly Ile Glu Phe Met Glu Ala Glu Glu
 260 265 270

 CTG TAC CAG AAG AGA GTG CTG ACC ATA ACC GGC ATC TGC 857
 Leu Tyr Gln Lys Arg Val Leu Thr Ile Thr Gly Ile Cys
 275 280 285

 ATC GCC CTC CTT GTG GTC GGC ATC ATG TGT GTG GTG GCC 896
 Ile Ala Leu Leu Val Val Gly Ile Met Cys Val Val Ala
 290 295

 TAC TGC AAA ACC AAG AAA CAG CGG AAA AAG CTG CAT GAC 935
 Tyr Cys Lys Thr Lys Lys Gln Arg Lys Lys Leu His Asp
 300 305 310

 CGT CTT CGG CAG AGC CTT CGG TCT GAA CGA AAC AAT ATG 974
 Arg Leu Arg Gln Ser Leu Arg Ser Glu Arg Asn Asn Met
 315 320

 ATG AAC ATT GCC AAT GGG CCT CAC CAT CCT AAC CCA CCC 1013
 Met Asn Ile Ala Asn Gly Pro His His Pro Asn Pro Pro
 325 330 335

FIG. 2B

CCC GAG AAT GTC CAG CTG GTG AAT CAA TAC GTA TCT AAA 1052
 Pro Glu Asn Val Gln Leu Val Asn Gln Tyr Val Ser Lys
 340 345 350

 AAC GTC ATC TCC AGT GAG CAT ATT GTT GAG AGA GAA GCA 1091
 Asn Val Ile Ser Ser Glu His Ile Val Glu Arg Glu Ala
 355 360

 GAG ACA TCC TTT TCC ACC AGT CAC TAT ACT TCC ACA GCC 1130
 Glu Thr Ser Phe Ser Thr Ser His Tyr Thr Ser Thr Ala
 365 370 375

 CAT CAC TCC ACT ACT GTC ACC CAG ACT CCT AGC CAC AGC 1169
 His His Ser Thr Thr Val Thr Gln Thr Pro Ser His Ser
 380 385

 TGG AGC AAC GGA CAC ACT GAA AGC ATC CTT TCC GAA AGC 1208
 Trp Ser Asn Gly His Thr Glu Ser Ile Leu Ser Glu Ser
 390 395 400

 CAC TCT GTA ATC GTG ATG TCA TCC GTA GAA AAC AGT AGG 1247
 His Ser Val Ile Val Met Ser Ser Val Glu Asn Ser Arg
 405 410 415

 CAC AGC AGC CCA ACT GGG GGC CCA AGA GGA CGT CTT AAT 1286
 His Ser Ser Pro Thr Gly Gly Pro Arg Gly Arg Leu Asn
 420 425

 GGC ACA GGA GGC CCT CGT GAA TGT AAC AGC TTC CTC AGG 1325
 Gly Thr Gly Gly Pro Arg Glu Cys Asn Ser Phe Leu Arg
 430 435 440

 CAT GCC AGA GAA ACC CCT GAT TCC TAC CGA GAC TCT CCT 1364
 His Ala Arg Glu Thr Pro Asp Ser Tyr Arg Asp Ser Pro
 445 450

 CAT AGT GAA AGG TAT GTG TCA GCC ATG ACC ACC CCG GCT 1403
 His Ser Glu Arg Tyr Val Ser Ala Met Thr Thr Pro Ala
 455 460 465

 CGT ATG TCA CCT GTA GAT TTC CAC ACG CCA AGC TCC CCC 1442
 Arg Met Ser Pro Val Asp Phe His Thr Pro Ser Ser Pro
 470 475 480

 AAA TCG CCC CCT TCG GAA ATG TCT CCA CCC GTG TCC AGC 1481
 Lys Ser Pro Pro Ser Glu Met Ser Pro Pro Val Ser Ser
 485 490

 ATG ACG GTG TCC ATG CCT TCC ATG GCG GTC AGC CCC TTC 1520
 Met Thr Val Ser Met Pro Ser Met Ala Val Ser Pro Phe
 495 500 505

ATG	GAA	GAA	GAG	AGA	CCT	CTA	CTT	CTC	GTG	ACA	CCA	CCA	1559
Met	Glu	Glu	Glu	Arg	Pro	Leu	Leu	CAT	CAC	CCT	CAG	CAG	
													510
AGG	CTG	CGG	GAG	AAG	TTC	GAC	CAT	CAC	CCT	CAG	CAG	CAG	1598
Arg	Leu	Arg	Glu	Lys									
													520
TTC	AGC	TCC	TTC	CAC	CAC	AAC	CCC	GCG	CAT	GAC	AGT	AAC	1637
Phe	Ser	Ser	Phe	His	His	Asn	Pro	Ala	His	Asp	Ser	Asn	
													535
AGC	CTC	CCT	GCT	AGC	CCC	TTG	AGG	ATA	GTG	GAG	GAT	GAG	1676
Ser	Leu	Pro	Ala	Ser	Pro	Leu	Arg	Ile	Val	Glu	Asp	Glu	
													540
GAG	TAT	GAA	ACG	ACC	CAA	GAG	TAC	GAG	CCA	GCC	CAA	GAG	1715
Glu	Tyr	Glu	Tyr	Thr	Gln	Glu	Tyr	Glu	Pro	Ala	Gln	Glu	
													550
CCT	GTT	AAG	AAA	CTC	GCC	AAT	AGC	CGG	CGG	GCC	AAA	AGA	1754
Pro	Val	Lys	Lys	Leu	Ala	Asn	Ser	Arg	Arg	Ala	Lys	Arg	
													560
ACC	AAG	CCC	AAT	GGC	CAC	ATT	GCT	AAC	AGA	TTG	GAA	GTG	1793
Thr	Lys	Pro	Asn	Gly	His	Ile	Ala	Asn	Arg	Leu	Glu	Val	
													585
GAC	AGC	AAC	ACA	AGC	TCC	CAG	AGC	AGT	AAC	TCA	GAG	AGT	1832
Asp	Ser	Ser	Asn	Thr	Ser	Ser	Gln	Ser	Ser	Asn	Ser	Ser	
													600
													610

FIG. 2D

GAA	ACA	GAA	GAT	GAA	AGA	GTA	GGT	GAA	GAT	ACG	CCT	TTC	1871
Glu	Thr	Glu	Asp	Glu	Arg	Val	Gly	Glu	Asp	Thr	Pro	Phe	
													620
CTG	GGC	ATA	CAG	AAC	CCC	CTG	GCA	GCC	AGT	CTT	GAG	GCA	1910
Leu	Gly	Ile	Gln	Asn	Pro	Leu	Ala	Ala	Ser	Leu	Glu	Ala	
													635
ACA	CCT	GCC	TTC	CGC	CTG	GCT	GAC	AGC	AGG	ACT	AAC	CCA	1949
Thr	Pro	Ala	Phe	Phe	Arg	Leu	Ala	Asp	Ser	Arg	Thr	Asn	
													640
GCA	GGC	CGC	TTC	TCG	ACA	CAG	GAA	GAA	ATC	CAG	GCC	AGG	1988
Ala	Gly	Gly	Phe	Ser	Thr	Gln	Glu	Glu	Ile	Gln	Ala	Arg	
													660
CTG	TCT	AGT	GTA	ATT	GCT	AAC	CAA	GAC	CCT	ATT	GCT	GTA	TA 2029
Leu	Ser	Ser	Val	Ile	Ala	Asn	Gln	Asp	Pro	Ile	Ala	Val	
													675
A	AACCTAAATA	AACACATAGA	TTCACCTGTA	AAACTTTATT									2070
TTATATAATA	AAGTATCCA	CCTTAATAA	AAACATTAT	TTTATTATTAG									2120
CAGTCTGCA	AATAGAAC	AGGAAAAAC	CTTTTATAAA	TTAAATATAT									2170
GTATGTAATA	ATGAAAAAA	AAAAAAA	AAAAAAA	AAAAAAA									2199

FIG. 2E

10/34

GTGGCTGCGG GGCAATTGAA AAAGAGCCGG CGAGGAGTTC CCCGAAACTT 50
GTTGGAACTC CGGGCTCGCG CGGAGGCCAG GAGCTGAGCG GC GGCGGCTG 100
CCGGACGATG GGAGCGTGAG CAGGACGGTG ATAACCTCTC CCCGATCGGG 150
TTGCGAGGGC GCCGGGCAGA GGCCAGGACG CGAGCCGCCA GC GGCGGGAC 200
CCATCGACGA CTTCCCGGGG CGACAGGAGC AGCCCCGAGA GCCAGGGCGA 250
GCGCCCGTTC CAGGTGGCCG GACCGCCCGC CGCGTCCGCG CC GCGCTCCC 300
TGCAGGCAAC GGGAGACGCC CCCGCGCAGC GCGAGCGCCT CAGCGCGGCC 350
GCTCGCTCTC CCCATCGAGG GACAAACTTT TCCCAAACCC GATCCGAGCC 400
CTTGGACCAA ACTCGCCTGC GCCGAGAGCC GTCCGCGTAG AGCGCTCCGT 450
CTCCGGCGAG ATG TCC GAG CGC AAA GAA GGC AGA GGC AAA 490
Met Ser Glu Arg Lys Glu Gly Arg Gly Lys
1 5 10
GGG AAG GGC AAG AAG AAG GAG CGA GGC TCC GGC AAG AAG 529
Gly Lys Gly Lys Lys Glu Arg Gly Ser Gly Lys Lys
15 20
CCG GAG TCC GCG GCG GGC AGC CAG AGC CCA GCC TTG CCT 568
Pro Glu Ser Ala Ala Gly Ser Gln Ser Pro Ala Leu Pro
25 30 35
CCC CAA TTG AAA GAG ATG AAA AGC CAG GAA TCG GCT GCA 607
Pro Gln Leu Lys Glu Met Lys Ser Gln Glu Ser Ala Ala
40 45
GGT TCC AAA CTA GTC CTT CGG TGT GAA ACC AGT TCT GAA 646
Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu
50 55 60
TAC TCC TCT CTC AGA TTC AAG TGG TTC AAG AAT GGG AAT 685
Tyr Ser Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn
65 70 75
GAA TTG AAT CGA AAA AAC AAA CCA CAA AAT ATC AAG ATA 724
Glu Leu Asn Arg Lys Asn Lys Pro Gln Asn Ile Lys Ile
80 85

FIG.3A

11/34

CAA AAA AAG CCA GGG AAG TCA GAA CTT CGC ATT AAC AAA 763
Gln Lys Lys Pro Gly Lys Ser Glu Leu Arg Ile Asn Lys
90 95 100

GCA TCA CTG GCT GAT TCT GGA GAG TAT ATG TGC AAA GTG 802
Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val
105 110

ATC AGC AAA TTA GGA AAT GAC AGT GCC TCT GCC AAT ATC 841
Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile
115 120 125

ACC ATC GTG GAA TCA AAC GAG ATC ATC ACT GGT ATG CCA 880
Thr Ile Val Glu Ser Asn Glu Ile Ile Thr Gly Met Pro
130 135 140

GCC TCA ACT GAA GGA GCA TAT GTG TCT TCA GAG TCT CCC 919
Ala Ser Thr Glu Gly Ala Tyr Val Ser Ser Glu Ser Pro
145 150

ATT AGA ATA TCA GTA TCC ACA GAA GGA GCA AAT ACT TCT 958
Ile Arg Ile Ser Val Ser Thr Glu Gly Ala Asn Thr Ser
155 160 165

TCA TCT ACA TCT ACA TCC ACC ACT GGG ACA AGC CAT CTT 997
Ser Ser Thr Ser Thr Ser Thr Gly Thr Ser His Leu
170 175

GTA AAA TGT GCG GAG AAG GAG AAA ACT TTC TGT GTG AAT 1036
Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
180 185 190

GGA GGG GAG TGC TTC ATG GTG AAA GAC CTT TCA AAC CCC 1075
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro
195 200 205

TCG AGA TAC TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT 1114
Ser Arg Tyr Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly
210 215

GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AAG 1153
Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Lys
220 225 230

GCG GAG GAG CTG TAC CAG AAG AGA GTG CTG ACC ATA ACC 1192
Ala Glu Glu Leu Tyr Gln Lys Arg Val Leu Thr Ile Thr
235 240

GGC ATC TGC ATC GCC CTC CTT GTG GTC GGC ATC ATG TGT 1231
Gly Ile Cys Ile Ala Leu Leu Val Val Gly Ile Met Cys
245 250 255

GTG GTG GCC TAC TGC AAA ACC AAG AAA CAG CGG AAA AAG 1270
Val Val Ala Tyr Cys Lys Thr Lys Lys Gln Arg Lys Lys
260 265 270

FIG. 3B

FIG. 3C

GTG TCC AGC ATG ACG GTG TCC AAG CCT TCC ATG GCG GTC 1855
 Val Ser Ser Met Thr Val Ser Lys Pro Ser Met Ala Val
 455 460 465

 AGC CCC TTC ATG GAA GAA GAG AGA CCT CTA CTT CTC GTG 1894
 Ser Pro Phe Met Glu Glu Glu Arg Pro Leu Leu Leu Val
 470 475

 ACA CCA CCA AGG CTG CGG GAG AAG AAG TTT GAC CAT CAC 1933
 Thr Pro Pro Arg Leu Arg Glu Lys Lys Phe Asp His His
 480 485 490

 CCT CAG CAG TTC AGC TCC TTC CAC CAC AAC CCC GCG CAT 1972
 Pro Gln Gln Phe Ser Ser Phe His His Asn Pro Ala His
 495 500

 GAC AGT AAC AGC CTC CCT GCT AGC CCC TTG AGG ATA GTG 2011
 Asp Ser Asn Ser Leu Pro Ala Ser Pro Leu Arg Ile Val
 505 510 515

 GAG GAT GAG GAG TAT GAA ACG ACC CAA GAG TAC GAG CCA 2050
 Glu Asp Glu Glu Tyr Glu Thr Thr Gln Glu Tyr Glu Pro
 520 525 530

 GCC CAA GAG CCT GTT AAG AAA CTC GCC AAT AGC CGG CGG 2089
 Ala Gln Glu Pro Val Lys Lys Leu Ala Asn Ser Arg Arg
 535 540

 GCC AAA AGA ACC AAG CCC AAT GGC CAC ATT GCT AAC AGA 2128
 Ala Lys Arg Thr Lys Pro Asn Gly His Ile Ala Asn Arg
 545 550 555

 TTG GAA GTG GAC AGC AAC ACA AGC TCC CAG AGC AGT AAC 2167
 Leu Glu Val Asp Ser Asn Thr Ser Ser Gln Ser Ser Asn
 560 565

 TCA GAG AGT GAA ACA GAA GAT GAA AGA GTA GGT GAA GAT 2206
 Ser Glu Ser Glu Thr Glu Asp Glu Arg Val Gly Glu Asp
 570 575 580

 ACG CCT TTC CTG GGC ATA CAG AAC CCC CTG GCA GCC AGT 2245
 Thr Pro Phe Leu Gly Ile Gln Asn Pro Leu Ala Ala Ser
 585 590 595

 CTT GAG GCA ACA CCT GCC TTC CGC CTG GCT GAC AGC AGG 2284
 Leu Glu Ala Thr Pro Ala Phe Arg Leu Ala Asp Ser Arg
 600 605

 ACT AAC CCA GCA GGC CGC TTC TCG ACA CAG GAA GAA ATC 2323
 Thr Asn Pro Ala Gly Arg Phe Ser Thr Gln Glu Glu Ile
 610 615 620

 CAG GCC AGG CTG TCT AGT GTA ATT GCT AAC CAA GAC CCT 2362
 Gln Ala Arg Leu Ser Ser Val Ile Ala Asn Gln Asp Pro
 625 630

FIG. 3D

ATT GCT GTA TAAAACCTA AATAAACACA TAGATTCACC TGTAAAACCTT 2410
Ile Ala Val
635 637

TATTTTATAT AATAAAGTAT TCCACCTTAA ATTAAACAAAT TTATTTTATT 2460

TTAGCAGTTC TGCAAATAAA AAAAAAAA 2490

FIG. 3E

GCGCCTGCCT CCAACCTGCG GGCAGGGAGGT GGGTGGCTGC GGGGCAATTG 50

AAAAAGAGCC GGCAGGGAGT TCCCCGAAAC TTGTTGGAAC TCCGGGCTCG 100

CGCGGAGGCC AGGAGCTGAG CGGCAGCGGC TGCCGGACGA TGGGAGCGTG 150

AGCAGGACGG TGATAACCTC TCCCCGATCG GGTTGCGAGG GCGCCGGGCA 200

GAGGCCAGGA CGCGAGCCGC CAGCGCGGG ACCCATCGAC GACTTCCCAGG 250

GGCGACAGGA GCAGCCCCGA GAGCCAGGGC GAGCGCCCGT TCCAGGTGGC 300

CGGACCGCCC GCCGCGTCCG CGCCGCGCTC CCTGCAGGCA ACGGGAGACG 350

CCCCCGCGCA GCGCGAGCGC CTCAGCGCGG CCGCTCGCTC TCCCCATCGA 400

GGGACAAACT TTTCCAAAC CCGATCCGAG CCCTTGGACC AAACCTGCCT 450

GCGCCGAGAG CCGTCCGCGT AGAGCGCTCC GTCTCCGGCG AG ATG 495
Met
1

TCC GAG CGC AAA GAA GGC AGA GGC AAA GGG AAG GGC AAG 534
Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys
5 10

AAG AAG GAG CGA GGC TCC GGC AAG AAG CCG GAG TCC GCG 573
Lys Lys Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala
15 20 25

GCG GGC AGC CAG AGC CCA GCC TTG CCT CCC CAA TTG AAA 612
Ala Gly Ser Gln Ser Pro Ala Leu Pro Pro Gln Leu Lys
30 35 40

GAG ATG AAA AGC CAG GAA TCG GCT GCA GGT TCC AAA CTA 651
Glu Met Lys Ser Gln Glu Ser Ala Ala Gly Ser Lys Leu
45 50

GTC CTT CGG TGT GAA ACC AGT TCT GAA TAC TCC TCT CTC 690
Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu
55 60 65

AGA TTC AAG TGG TTC AAG AAT GGG AAT GAA TTG AAT CGA 729
Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg
70 75

FIG. 4A

16/34

AAA AAC AAA CCA CAA AAT ATC AAG ATA CAA AAA AAG CCA 768
Lys Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro
80 85 90

GGG AAG TCA GAA CTT CGC ATT AAC AAA GCA TCA CTG GCT 807
Gly Lys Ser Glu Leu Arg Ile Asn Lys Ala Ser Leu Ala
95 100 105

GAT TCT GGA GAG TAT ATG TGC AAA GTG ATC AGC AAA TTA 846
Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys Leu
110 115

GGA AAT GAC AGT GCC TCT GCC AAT ATC ACC ATC GTG GAA 885
Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu
120 125 130

TCA AAC GAG ATC ATC ACT GGT ATG CCA GCC TCA ACT GAA 924
Ser Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu
135 140

GGA GCA TAT GTG TCT TCA GAG TCT CCC ATT AGA ATA TCA 963
Gly Ala Tyr Val Ser Ser Glu Ser Pro Ile Arg Ile Ser
145 150 155

GTA TCC ACA GAA GGA GCA AAT ACT TCT TCA TCT ACA TCT 1002
Val Ser Thr Glu Gly Ala Asn Thr Ser Ser Ser Thr Ser
160 165 170

ACA TCC ACC ACT GGG ACA AGC CAT CTT GTA AAA TGT GCG 1041
Thr Ser Thr Thr Gly Thr Ser His Leu Val Lys Cys Ala
175 180

GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGG GAG TGC 1080
Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys
185 190 195

TTC ATG GTG AAA GAC CTT TCA AAC CCC TCG AGA TAC TTG 1119
Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu
200 205

TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA 1158
Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln
210 215 220

AAC TAC GTA ATG GCC AGC TTC TAC AGT ACG TCC ACT CCC 1197
Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro
225 230 235

TTT CTG TCT CTG CCT GAA TAGGA GCATGCTCAG TTGGTGCTGC 1240
Phe Leu Ser Leu Pro Glu
240 241

TTTCTTGTG CTGCATCTCC CCTCAGATTC CACCTAGAGC TAGATGTGTC 1290

FIG. 4B

TTACCAGATC TAATATTGAC TGCCTCTGCC TGTCGCATGA GAACATTAAC 1340
AAAAGCAATT GTATTACTTC CTCTGTTCGC GACTAGTTGG CTCTGAGATA 1390
CTAATAGGTG TGTGAGGCTC CGGATGTTTC TGGAATTGAT ATTGAATGAT 1440
GTGATACAAA TTGATAGTCA ATATCAAGCA GTGAAATATG ATAATAAAGG 1490
CATTTCAAAG TCTCACTTT ATTGATAAAA TAAAAATCAT TCTACTGAAC 1540
AGTCCATCTT CTTTATACAA TGACCACATC CTGAAAAGGG TGTTGCTAAG 1590
CTGTAACCGA TATGCACTTG AAATGATGGT AAGTTAATT TGATTCAGAA 1640
TGTGTTATTT GTCACAAATA AACATAATAA AAGGAGTTCA GATGTTTTC 1690
TTCATTAACC AAAAAAAAAA AAAAAA 1715

FIG. 4C

GAGGCGCCCTG CCTCCAACCT GCGGGCGGGGA GGTGGGTGGC TGCGGGGCAA 50
TTGAAAAAGA GCCGGCGAGG AGTTCCCCGA AACTTGTGAA AACTCCGGGC 100
TCGCGCGGAG GCCAGGAGCT GAGCGCGGGC GGCTGCCGGA CGATGGGAGC 150
GTGAGCAGGA CGGTGATAAC CTCTCCCCGA TCGGGTTGCG AGGGCGCCGG 200
GCAGAGGCCA GGACGCGAGC CGCCAGCGGC GGGACCCATC GACGACTTCC 250
CGGGGCGACA GGAGCAGCCC CGAGAGCCAG GGCGAGCGCC CGTTCCAGGT 300
GGCCGGACCG CCCGCCGCGT CCGCGCCGCG CTCCCTGCAG GCAACGGGAG 350
ACGCCCGCGC GCAGCGCGAG CGCCTCAGCG CGGCCGCTCG CTCTCCCCAT 400
CGAGGGACAA ACTTTTCCCA AACCCGATCC GAGCCCTTGG ACCAAACTCG 450
CCTGCGCCGA GAGCCGTCCG CGTAGAGCGC TCCGTCTCCG GCGAG AT 497
Met 1
G TCC GAG CGC AAA GAA GGC AGA GGC AAA GGG AAG GGC AAG 537
Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys
5 10
AAG AAG GAG CGA GGC TCC GGC AAG AAG CCG GAG TCC GCG 576
Lys Lys Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala
15 20 25
GCG GGC AGC CAG AGC CCA GCC TTG CCT CCC CAA TTG AAA 615
Ala Gly Ser Gln Ser Pro Ala Leu Pro Pro Gln Leu Lys
30 35 40
GAG ATG AAA AGC CAG GAA TCG GCT GCA GGT TCC AAA CTA 654
Glu Met Lys Ser Gln Glu Ser Ala Ala Gly Ser Lys Leu
45 50
GTC CTT CGG TGT GAA ACC AGT TCT GAA TAC TCC TCT CTC 693
Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu
55 60 65
AGA TTC AAG TGG TTC AAG AAT GGG AAT GAA TTG AAT CGA 732
Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg
70 75

FIG. 5A

AAA AAC AAA CCA CAA AAT ATC AAG ATA CAA AAA AAG CCA 771
 Lys Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro
 80 85 90

GGG AAG TCA GAA CTT CGC ATT AAC AAA GCA TCA CTG GCT 810
 Gly Lys Ser Glu Leu Arg Ile Asn Lys Ala Ser Leu Ala
 95 100 105

GAT TCT GGA GAG TAT ATG TGC AAA GTG ATC AGC AAA TTA 849
 Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys Leu
 110 115

GGA AAT GAC AGT GCC TCT GCC AAT ATC ACC ATC GTG GAA 888
 Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu
 120 125 130

TCA AAC GAG ATC ATC ACT GGT ATG CCA GCC TCA ACT GAA 927
 Ser Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu
 135 140

GGA GCA TAT GTG TCT TCA GAG TCT CCC ATT AGA ATA TCA 966
 Gly Ala Tyr Val Ser Ser Glu Ser Pro Ile Arg Ile Ser
 145 150 155

GTA TCC ACA GAA GGA GCA AAT ACT TCT TCA TCT ACA TCT 1005
 Val Ser Thr Glu Gly Ala Asn Thr Ser Ser Ser Thr Ser
 160 165 170

ACA TCC ACC ACT GGG ACA AGC CAT CTT GTA AAA TGT GCG 1044
 Thr Ser Thr Thr Gly Thr Ser His Leu Val Lys Cys Ala
 175 180

GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGG GAG TGC 1083
 Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys
 185 190 195

TTC ATG GTG AAA GAC CTT TCA AAC CCC TCG AGA TAC TTG 1122
 Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu
 200 205

TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA 1161
 Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln
 210 215 220

AAC TAC GTA ATG GCC AGC TTC TAC AAG GCG GAG GAG CTG 1200
 Asn Tyr Val Met Ala Ser Phe Tyr Lys Ala Glu Glu Leu
 225 230 235

TAC CAG AAG AGA GTG CTG ACC ATA ACC GGC ATC TGC ATC 1239
 Tyr Gln Lys Arg Val Leu Thr Ile Thr Gly Ile Cys Ile
 240 245

GCC CTC CTT GTG GTC GGC ATC ATG TGT GTG GTG GCC TAC 1278
 Ala Leu Leu Val Val Gly Ile Met Cys Val Val Ala Tyr
 250 255 260

TGC AAA ACC AAG AAA CAG CGG AAA AAG CTG CAT GAC CGT 1317
 Cys Lys Thr Lys Lys Gln Arg Lys Lys Leu His Asp Arg
 265 270

 CTT CGG CAG AGC CTT CGG TCT GAA CGA AAC AAT ATG ATG 1356
 Leu Arg Gln Ser Leu Arg Ser Glu Arg Asn Asn Met Met
 275 280 285

 AAC ATT GCC AAT GGG CCT CAC CAT CCT AAC CCA CCC CCC 1395
 Asn Ile Ala Asn Gly Pro His His Pro Asn Pro Pro Pro
 290 295 300

 GAG AAT GTC CAG CTG GTG AAT CAA TAC GTA TCT AAA AAC 1434
 Glu Asn Val Gln Leu Val Asn Gln Tyr Val Ser Lys Asn
 305 310

 GTC ATC TCC AGT GAG CAT ATT GTT GAG AGA GAA GCA GAG 1473
 Val Ile Ser Ser Glu His Ile Val Glu Arg Glu Ala Glu
 315 320 325

 ACA TCC TTT TCC ACC AGT CAC TAT ACT TCC ACA GCC CAT 1512
 Thr Ser Phe Ser Thr Ser His Tyr Thr Ser Thr Ala His
 330 335

 CAC TCC ACT ACT GTC ACC CAG ACT CCT AGC CAC AGC TGG 1551
 His Ser Thr Thr Val Thr Gln Thr Pro Ser His Ser Trp
 340 345 350

 AGC AAC GGA CAC ACT GAA AGC ATC CTT TCC GAA AGC CAC 1590
 Ser Asn Gly His Thr Glu Ser Ile Leu Ser Glu Ser His
 355 360 365

 TCT GTA ATC GTG ATG TCA TCC GTA GAA AAC AGT AGG CAC 1629
 Ser Val Ile Val Met Ser Ser Val Glu Asn Ser Arg His
 370 375

 AGC AGC CCA ACT GGG GGC CCA AGA GGA CGT CTT AAT GGC 1668
 Ser Ser Pro Thr Gly Gly Pro Arg Gly Arg Leu Asn Gly
 380 385 390

 ACA GGA GGC CCT CGT GAA TGT AAC AGC TTC CTC AGG CAT 1707
 Thr Gly Gly Pro Arg Glu Cys Asn Ser Phe Leu Arg His
 395 400

 GCC AGA GAA ACC CCT GAT TCC TAC CGA GAC TCT CCT CAT 1746
 Ala Arg Glu Thr Pro Asp Ser Tyr Arg Asp Ser Pro His
 405 410 415

 AGT GAA AGG TAAAAA CCGAAGGCAA AGCTACTGCA GAGGAGAAC 1790
 Ser Glu Arg
 420

FIG. 5C

TCAGTCAGAG AATCCCTGTG AGCACCTGCG GTCTCACCTC AGGAAATCTA 1840
CTCTAACATCAG AATAAGGGGC GGCAGTTACC TGTTCTAGGA GTGCTCCTAG 1890
TTGATGAACT CATCTCTTG TTTGACGGAA CTTATTTCTT CTGAGCTTCT 1940
CTCGTCGTCC CAGTGACTGA CAGGCAACAG ACTCTTAAAG AGCTGGGATG 1990
CTTGATGCG GAAGGTGCAG CACATGGAGT TTCCAGCTCT GCCATGGGC 2040
TCAGACCCAC TCGGGGTCTC AGTGTCCCTCA GTTGTAACAT TAGAGAGATG 2090
GCATCAATGC TTGATAAGGA CCCTTCTATA ATTCCAATTG CCAGTTATCC 2140
AAACTCTGAT TCGGTGGTCG AGCTGCCCTC GTGTTCTTAT CTGCTAACCC 2190
TGTCTTACCT TCCAGCCTCA GTTAAGTCAA ATCAAGGGCT ATGTCATTGC 2240
TGAATGTCAT GGGGGCAAC TGCTTGCCCT CCACCTATA GTATCTATT 2290
TATGAAATTC CAAGAAGGGA TGAATAAATA AATCTCTGG ATGCTGCGTC 2340
TGGCAGTCTT CACGGGTGGT TTTCAAAGCA GAAAAAAA AAAAAAAA 2390
AAAAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA A 2431

FIG. 5D

16	1	M S E R K E G R G K G K K K E R G S G K K P E S A A G S Q S P A L P P R L K E M K S Q E S A A G	
11	1	M S E R K E G R G K G K K K E R G S G K K P E S A A G S Q S P A L P P Q L K E M K S Q E S A A G	
76	1	M S E R K E G R G K G K K K E R G S G K K P E S A A G S Q S P A L P P Q L K E M K S Q E S A A G	
84	1	M S E R K E G R G K G K K K E R G S G K K P E S A A G S Q S P A L P P Q L K E M K S Q E S A A G	
78	1	M S E R K E G R G K G K K K E R G S G K K P E S A A G S Q S P A L P P Q L K E M K S Q E S A A G	
16	51	S K L V L R C E T S S E Y S S L R F K W F K N G N E L N R K N K P Q N I K I Q K K P G K S E L R I N	
11	51	S K L V L R C E T S S E Y S S L R F K W F K N G N E L N R K N K P Q N I K I Q K K P G K S E L R I N	
76	51	S K L V L R C E T S S E Y S S L R F K W F K N G N E L N R K N K P Q N I K I Q K K P G K S E L R I N	
84	51	S K L V L R C E T S S E Y S S L R F K W F K N G N E L N R K N K P Q N I K I Q K K P G K S E L R I N	
78	51	S K L V L R C E T S S E Y S S L R F K W F K N G N E L N R K N K P Q N I K I Q K K P G K S E L R I N	
16	101	K A S L A D S G E Y M C K V I S K L G N D S A S A N I T I V E S N E I I T G M P A S T E G A Y V S S	
11	101	K A S L A D S G E Y M C K V I S K L G N D S A S A N I T I V E S N E I I T G M P A S T E G A Y V S S	
76	101	K A S L A D S G E Y M C K V I S K L G N D S A S A N I T I V E S N E I I T G M P A S T E G A Y V S S	
84	101	K A S L A D S G E Y M C K V I S K L G N D S A S A N I T I V E S N E I I T G M P A S T E G A Y V S S	
78	101	K A S L A D S G E Y M C K V I S K L G N D S A S A N I T I V E S N E I I T G M P A S T E G A Y V S S	
16	151	E S P I R I S V S T E G A N T S S S T S T T G T S H L V K C A E K E K T F C V N G G E C F M V K	
11	151	E S P I R I S V S T E G A N T S S S T S T T G T S H L V K C A E K E K T F C V N G G E C F M V K	
76	151	E S P I R I S V S T E G A N T S S S T S T T G T S H L V K C A E K E K T F C V N G G E C F M V K	
84	151	E S P I R I S V S T E G A N T S S S T S T T G T S H L V K C A E K E K T F C V N G G E C F M V K	
78	151	E S P I R I S V S T E G A N T S S S T S T T G T S H L V K C A E K E K T F C V N G G E C F M V K	

FIG. 6A

16	201	DLSNPSRYLCKCQPGFTGARCTEN[VPMKVQNQ]- - -	EKAEEELYQKRVLT
11	201	DLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFME	AEEELYQKRVLT
76	201	DLSNPSRYLCKCPNEFTGDRCQNYVMASFYK-	AEEELYQKRVLT
84	201	DLSNPSRYLCKCPNEFTGDRCQNYVMASFYK-	AEEELYQKRVLT
78	201	DLSNPSRYLCKCPNEFTGDRCQNYVMASFY[STSTPFLSLPE]	
16	246	ITGICIALLVVGIMCVVAYCKTKQRKKLHDRLRQSLRSERNMMNIANG	
11	251	ITGICIALLVVGIMCVVAYCKTKQRKKLHDRLRQSLRSERNMMNIANG	
76	243	ITGICIALLVVGIMCVVAYCKTKQRKKLHDRLRQSLRSERNMMNIANG	
84	243	ITGICIALLVVGIMCVVAYCKTKQRKKLHDRLRQSLRSERNMMNIANG	
16	296	PHHPNPPENVQLVNQYVSKNVISSEHIVEREAEATSFSSTSHTSTAHHST	
11	301	PHHPNPPENVQLVNQYVSKNVISSEHIVEREAEATSFSSTSHTSTAHHST	
76	293	PHHPNPPENVQLVNQYVSKNVISSEHIVEREAEATSFSSTSHTSTAHHST	
84	293	PHHPNPPENVQLVNQYVSKNVISSEHIVEREAEATSFSSTSHTSTAHHST	
16	346	TVTQTPSHSWNGHTESILSESSHSSVIVMSSVENSRHSSPTGGPRGRLLNGT	
11	351	TVTQTPSHSWNGHTESILSESSHSSVIVMSSVENSRHSSPTGGPRGRLLNGT	
76	343	TVTQTPSHSWNGHTESILSESSHSSVIVMSSVENSRHSSPTGGPRGRLLNGT	
84	343	TVTQTPSHSWNGHTESILSESSHSSVIVMSSVENSRHSSPTGGPRGRLLNGT	

FIG. 6B

16	396	G G P R E C N S F L R H A R E T P D S Y R D S P H S E R Y V S A M T T P A R M S P V D F H T P S S P
11	401	G G P R E C N S F L R H A R E T P D S Y R D S P H S E R Y V S A M T T P A R M S P V D F H T P S S P
76	393	G G P R E C N S F L R H A R E T P D S Y R D S P H S E R Y V S A M T T P A R M S P V D F H T P S S P
84	393	G G P R E C N S F L R H A R E T P D S Y R D S P H S E R - - - - -
16	446	K S P P S E M S P P V S S M T V S M P S M A V S P F M E E E R P L L V T P P R L R E K K F D H H P
11	451	K S P P S E M S P P V S S M T V S M P S M A V S P F M E E E R P L L V T P P R L R E K K F D H H P
76	443	K S P P S E M S P P V S S M T V S K P S M A V S P F M E E E R P L L V T P P R L R E K K F D H H P
16	496	Q Q F S S F H H N P A H D S N S L P A S P L R I V E D E E Y E T T Q E Y E P A Q E P V K K L A N S R
11	501	Q Q F S S F H H N P A H D S N S L P A S P L R I V E D E E Y E T T Q E Y E P A Q E P V K K L A N S R
76	493	Q Q F S S F H H N P A H D S N S L P A S P L R I V E D E E Y E T T Q E Y E P A Q E P V K K L A N S R
16	546	R A K R T K P N G H I A N R L E V D S N T S S Q S S N S E S E T E D E R V G E D T P F L G I Q N P L
11	551	R A K R T K P N G H I A N R L E V D S N T S S Q S S N S E S E T E D E R V G E D T P F L G I Q N P L
76	543	R A K R T K P N G H I A N R L E V D S N T S S Q S S N S E S E T E D E R V G E D T P F L G I Q N P L
16	596	A A S L E A T P A F R L A D S R T N P A G R F S T Q E E I Q - - - - -
11	601	A A S L E A T P A F R L A D S R T N P A G R F S T Q E E I Q A R L S S V I A N Q D P I A V
76	593	A A S L E A T P A F R L A D S R T N P A G R F S T Q E E I Q A R L S S V I A N Q D P I A V

Fig. 6C

1 GGGTACCATGGTCGGTGAGCGCGTTCCCGCTGAGCGCAACTAGCGGC
51 GGGTCGTGGCACCTCCAGAAAAGATCCCGCACCCTCCAGGATCAA
101 TGGCCTGGAGAGAGGGCTGCAGGGCCACGGACATTGCTGACTCTTCAG
151 AACGTGCTGACATGGAGGCCAGGTAGACTGAAATTATCATGTGTCCAAATT
201 AAAATTGCATACTTCAAGGATTATTGAAGGACTATTCTTAGACCCTTT
251 AAGAAGATTAAAGAAAAACACTCGGCCCTGAGTGCAGGAGGACCCCTG

301 TTTGTGGATGTGGAGGAGCGCGGGCCGGAGGCCATGGACGTGAAGGAGAG
1 M D V K E R

351 GAAGCCTTACCGCTCGCTGACCCGGCGCCGACGCCGAGCGCCGCTACA
7 K P Y R S L T R R R D A E R R Y T

401 CCAGCTCGTCCGGACAGCGAGGGCAAAGCCCCGAGAAATCGTAC
24 S S S A D S E E G K A P Q K S Y

451 AGCTCCAGCGAGAACCTGAAGGCCTACGACCAGGACGCCGCTAGCCTA
40 S S S E T L K A Y D Q D A R L A Y

501 TGGCAGCCGCGTCAAGGACATTGTGCCGCAGGAGGCCGAGGAATTCTGCC
57 G S R V K D I V P Q E A E E F C R

•
551 GCACAGGTGCCAACTTCACCCCTGCGGGAGCTGGGGCTGGAAGAAGTAACG
74 T G A N F T L R E L G L E E V T

601 CCCCCCTCACGGGACCCCTGTACCGGACAGACATTGGCCTCCCCACTGCGG
90 P P H G T L Y R T D I G L P H C G

651 CTACTCCATGGGGCTGGCTCTGATGCCGACATGGAGGCTGACACCGTGC
107 Y S M G A G S D A D M E A D T V L

701 TGTCCCCCTGAGCACCCCGTGCCTGTGTGGGCCGGAGCACACGGTCAGGG
124 S P E H P V R L W G R S T R S G

•
751 CGCAGCTCCTGCCGTCCAGCCGGCCAATTCCAATCTCACACTCACCGA
140 R S S C L S S R A N S N L T L T D

801 CACCGAGCATGAAAACACTGAGACTGATCATCCGGCGGCCCTGCAGAAC
157 T E H E N T E T D H P G G L Q N H

851 ACGCGCGGCTCCGGACGCCGCCGCCGCTCTGCACGCCACACCCCC
174 A R L R T P P P P L S H A H T P

901 AACCAAGCACCGCGGCCTCCATTAACTCCCTGAACCGGGCAACTTCAC
190 N Q H H A A S I N S L N R G N F T

951 GCCGAGGAGCAACCCCAGCCGGCCCCACGGACCACTCGCTCTCCGGAG
207 P R S N P S P A P T D H S L S G E

1001 AGCCCCCTGCCGGCGGCCAGGAGCCTGCCACGCCAGGAGAACTGG
224 P P A G G A Q E P A H A Q E N W

1051 CTGCTAACAGCAACATCCCCCTGGAGACCAAGAAACCTAGGCAAGCAGCC
240 L L N S N I P L E T R N L G K Q P

FIG. 7A

2001 CACCACTGCCATTGCCTTGCCTCCCCGATTGAAAGAGATGAAAAGCCAGG
 557 T T A I A L P P R L K E M K S Q E

 2051 AATCGGCTGCAGGTTCAAACACTAGTCCTCGGTGTGAAACCAGTTCTGAA
 574 S A A G S K L V L R C E T S S E

 2101 TACTCCTCTCTCAGATTCAAGTGTTCAAGAATGGGAATGAATTGAATCG
 590 Y S S L R F K W F K N G N E L N R

 2151 AAAAAACAAACCAACAAATATCAAGATAACAAAAAGCCAGGGAAGTCAG
 607 K N K P Q N I K I Q K K P G K S E

 2201 AACTTCGCATTAACAAAGCATCACTGGCTGATTCTGGAGAGTATATGTGC
 624 L R I N K A S L A D S G E Y M C
 •
 2251 AAAGTGATCAGCAAATTAGGAAATGACAGTGCCTCTGCCAATATCACCAT
 640 K V I S K L G N D S A S A N I T I

 2301 CGTCCAATCAAACGAGATCATCACTGGTATGCCAGCCTCAACTGAAGGGAG
 657 V E S N E I I T G M P A S T E G A

 2351 CATATGTGTCTTCAGAGTCTCCCATTAGAATATCAGTATCCACAGAACAGGA
 674 Y V S S E S P I R I S V S T E G
 •
 2401 GCAAATACTTCTTCATCTACATCTACATCCACCACTGGGACAAGCCATCT
 690 A N T S S S T S T S T G T S H L

 2451 TGAAAATGTGGGAGAAGGGAGAAAACCTTCTGTGTGAATGGACGGGAGT
 707 V K C A E K E K T F C V N G G E C

 2501 GCTCATGGTGAAAGACCTTCAAACCCCTCGAGATACTTGTGCAAGTGC
 724 F M V K D L S N P S R Y L C K C

 2551 CCAAATGAGTTACTGGTATCGCTGCCAAACTACGTAATGCCAGCTT
 740 P N E F T G D R C Q N Y V M A S F

 2601 CTACAGTACGTCCACTCCCTTCTGTCTGCCTGAATAGGAGCATGCTC
 757 Y S T S T P F L S L P E

 2651 AGTTGGTGCTGTTCTTGTGCTGCATCTCCCTCAGATTCCACCTAGA

 2701 GCTAGATGTGTCTTACCAAGATCTAATATTGACTGCCCTGCCTGTCGCAT
 2751 GAGAACATTAACAAAGCAATTGTATTACTTCCTCTGTTCGCGACTAGTT
 2801 GGCTCTGAGATACTAATAGGTGTGAGGCTCCGGATTTCTGGAATTG
 2851 ATATTGAATGATGTGATACAAATTGATAGTCATATCAAGCAGTGAATA
 2901 TGATAATAAAGGCATTCAAAGTCTCACTTTATTGATAAAATAAAATC
 2951 ATTCTACTGAACAGTCCATCTCTTATACAATGACCAACATCCTGAAAAG
 3001 GGTGTTGCTAAGCTGTAACCGATATGCACTGAAATGATGGTAAGTTAAT
 3051 TTTGATTCAAGAATGTGTTATTGTACAAATAACATAATAAAAGGAAAA
 3101 AAAAAAA

1101 ATTCCCTAGGGACATTGCAGGACAACCTCATTGAGATGGACATTCTCGGCG
 257 F L G T L Q D N L I E M D I L G A

 1151 CCTCCCGCCATGATGGGGCTTACAGTGACGGGCACTTCCTCTTCAAGCCT
 274 S R H D G A Y S D G H F L F K P

 1201 GGAGGCACCTCCCCGCTCTCTGCACCACATCACCAAGGGTACCCACTGAC
 290 G G T S P L F C T T S P G Y P L T

 1251 GTCCAGCACAGTGTACTCTCCCTCGCCCCGACCCCTGCCCGCAGCACCT
 307 S S T V Y S P P R P L P R S T F

 1301 TCGCCC GGCCGGCCTTAACCTCAAGAAGCCCTCCAAGTACTGTA ACTGG
 324 A R P A F N L K K P S K Y C N W

 1351 AAGTGCAGCCCTGAGCGCCATCGTCATCTCAGCCACTCTGGTCATCCT
 340 K C A A L S A I V I S A T L V I L

 1401 GCTGGCATACTTTGTGGCCATGCACCTGTTGGCTAAACTGGCACCTGC
 357 L A Y F V A M H L F G L N W H L Q

 1451 AGCCGATGGAGGGGCAGATGTATGAGATCACGGAGGACACAGCCAGCAGT
 374 P M E G Q M Y E I T E D T A S S

 1501 TGGCCTGTGCCAACCGACGTCTCCCTATACCCCTCAGGGGGCACTGGCTT
 390 W P V P T D V S L Y P S G G T G L

 1551 AGAGACCCCTGACAGGAAAGGCAAAGGAACCACAGAAGGAAAGCCCAGTA
 407 E T P D R K G K G T T E G K P S S

 1601 GTTCTTCCAGAGGACAGTTCATAGATTCTGGAGAAATTGATGTGGGA
 424 F F P E D S F I D S G E I D V G

 1651 AGGCGAGCTTCCCAGAAGATTCCCTGGCACTTCTGGAGATCTCAAGT
 440 R R A S Q K I P P G T F W R S Q V

 1701 GTTCATAGACCATCCTGTGCATCTGAAATTCAATGTGTCTCTGGAAAGG
 457 F I D H P V H L K F N V S L G K A

 1751 CAGCCCTGGTTGGCATTATGGCAGAAAAGGCCTCCCTCCTCACATACA
 474 A L V G I Y G R K G L P P S H T

 1801 CAGTTGACTTGTGGAGCTGGATGGCAGGAGGCTCCTAACCCAGGA
 490 Q F D F V E L L D G R R L L T Q E

 1851 GGC CGGGAGCCTAGAGGGACCCCGCGCCAGTCTCGGGAACTGTGCC
 507 A R S L E G T P R Q S R G T V P P

 1901 CCTCCAGCCATGAGACAGGCTTCATCCAGTATTGGATTCAAGGAATCTGG
 524 S S H E T G F I Q Y L D S G I W

 1951 CACTGGCTTTACAATGACGGAAAGGAGTCAGAAGTGGTTCTTCT
 540 H L A F Y N D G K E S E V V S F L

1 GAATTGGGACAGCCTCTGCCGCCGCTGCTGCTGCCGCCGCCACCGCCGGCTGGTCCCTCTGCTT
 76 TACTTCCTGCATGACAGTTGTTCTTCATCTGAGCAGACACCAGCTTCAGATGCTGAGGTGAGAAACATGC
 151 CTTTCAGTTGGCTACTGGTTACTTAATTAACTCAGCCGGCAGCTCCGTCGATCTATTTCGTCCTGTCCCT
 226 TGACGAGCCCAGGATGGTTGGAGTAGCATTTAAAAGAACTAGAAAAGTGGCCAGAAAACACCCAGCTTAAAGAAT
 301 TATTACGATATACTTGATTTGATTTGAGTTGCTAGGAGCTTCTTCCCCCTTGCATTTCTGAACCTTCTGA
 376 TTGTTAAATAATGGCCTGGACTTGGACGATTATCGATTCCCCCTGTAAGATGCTGTATCATTTGGTTGGGGGG
 451 CCTCTGCGTGGTAATGGACCGTGAGAGCGGCCAGGCCTCTCTGGAGGTGAGCCGATGGAGATTATTCCCCAG
 1 M E I Y S P D
 526 ACATGTCCTGAGGTGCCGCCGAGAGGTCCAGGCCACTCAGCTGAGTGAGACGCCATCTTGATGGC
 8 M S E V A A E R S S S P S T Q L S A D P S L D G L
 601 TTCCGGCAGCAGAACATGCCAGAGGCCAGACTGAAGATGGAGAACCCCTGGACTCGTGGCCCTGGCCGTC
 33 P A A E D M P E P Q T E D G R T P G L V G L A V P
 676 CCTGCTGCGTGGCTAGAACGCTGAGCGCCCTGAGAGGTGGCTCAACTCAGAGAAAAATCTGCATTGTC
 58 C A C L E A E R L R G C L N S E K I C I V P I L
 751 TGGCTTGCCCTGGTCAGCCCTGCCTCTGCATGCCGCCCTCAAGTGGTATTGTGGACAAGATCTTGAATATG
 83 A C L V S L C L C I A G L K W V F V D K I F E Y D
 826 ACTCTCTACTCACCTTGACCCCTGGGGCTTAGGCCAGGACCCATTATTTCTGGACCGAACCTGCTGCC
 108 S P T H L D P G G L G Q D P I I S L D A T A A S A
 901 CTGCTGGGTGTCGCTGAGGCATACACTTCACCTGCTCTAGGGCTCAATCTGAAGATGAGGTTCAAGTACAG
 133 V W V S S E A Y T S P V S R A Q S E S E V Q V T V
 976 TGCAAGGTGACAAGGCTGTTGCTCCTTGAACCATCAGGGCACCGAACCGAAGAACGTTGGCTTT
 158 Q G D K A V V S F E P S A A P T P K N R I F A F S
 1051 CTTCTTGCCG1CCACTGCGCCATCTCCCTCACCCACCCGGAACCCCTGAGGTGAGAACGCCAAGTCAGCAA
 183 F L P S T A P S F P S P T R N P E V R T P K S A T
 1126 CTCAGCCACAAACAACAGAAAATACTCCAAACTGCTCCTAAACTTCTACATCTACATCCACCAACTGGGACAA
 208 Q P Q T T E T N L Q T A P K L S T S T S T G T S
 1201 GCCATTTGAAATGTGGAGAAGGAGAAAACCTTCTGCTGAATGGAGGGAGTGCCTCATGGTAAAGACC
 233 H L V K C A E K E K T F C V N G G E C F M V K D L
 1276 TTTCACCCCTCGAGATACTTGTGCAAGTGGCCAAATGAGTTACTGGTGTGCTGCCAAACTACGTAATGG
 258 S N P S R Y L C K C P N E F T G D R C Q N Y V M A
 1351 CCAGCTTCTACAGTACGTCCACTCCCTTCTGCTCTGCCCTGAATAGGAGCATGCTCAGTTGGTGTGCTTCTT
 283 S F Y S T S T P F L S L P E O
 1426 GTTGTGCACTCCCTCAGATCCACCTAGAGCTAGATGCTCTTACCAAGATCTAAATTGACTGCCCTGCCT
 1501 GTCGCATGAGAACATTAACAAAGCAATTGATTACTTCCCTGTTGCGACTAGTTGGCTCTGAGATACTAATA
 1576 GGTGTGTGAGGCTCCGATGTTCTGGAATTGATATTGAATGATGTGATACAAATTGATAGTCAATATCAAGCAG
 1651 TGAAATATGATAATAAGGCATTTCAAAGTCTCACTTTATTGATAAAAATAAAATCATTCTACTGAACAGTCCA
 1726 TCTTCTTATACAAATGACCACATCCTGAAAAGGGTGTGCTAAGCTGTAACCGATATGCACTTGAATGATGGTA
 1801 AGTTAATTGATTGAGTCAGAATGTGTTATTGTCACAAATAACATAATAAAAAGGAAAAACCCGAATTG

EGF
-like

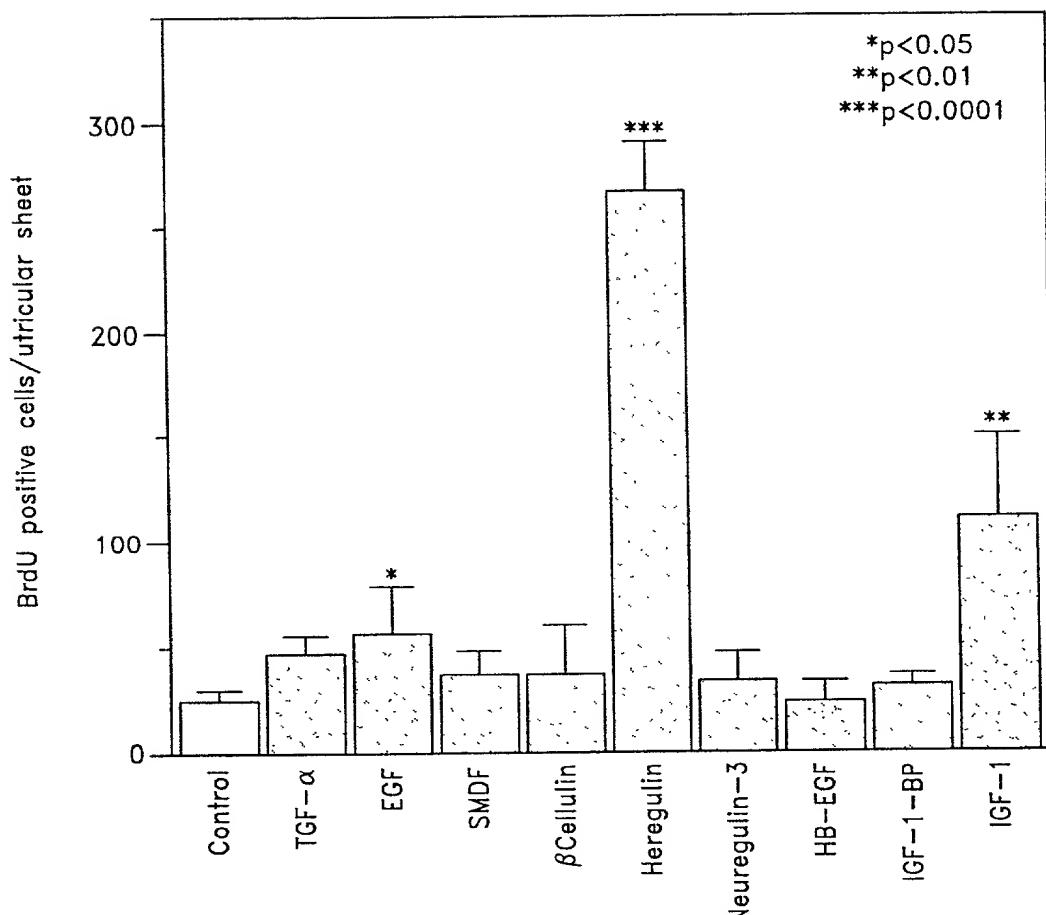


FIG. 9

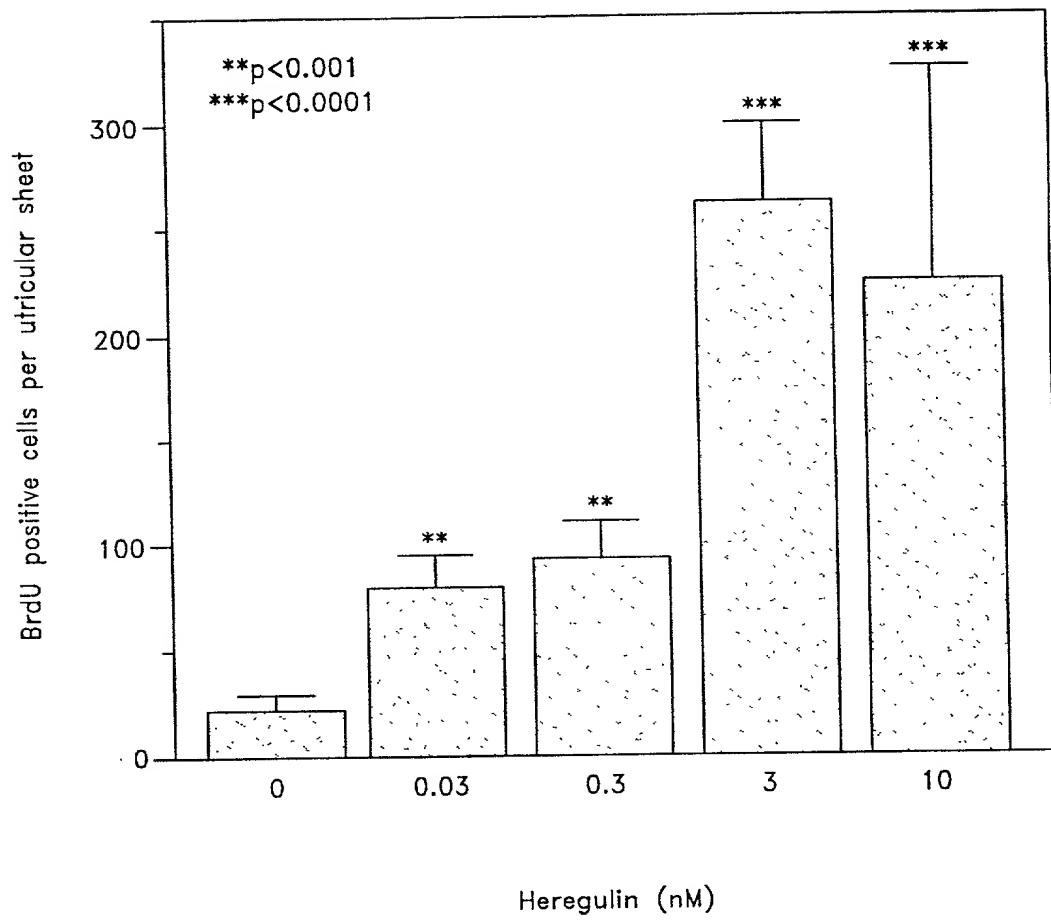


FIG. 10

Heregulin increases the number of 3H-thymidine labeled cells in supporting and hair cell layers in gentamicin-treated utricles

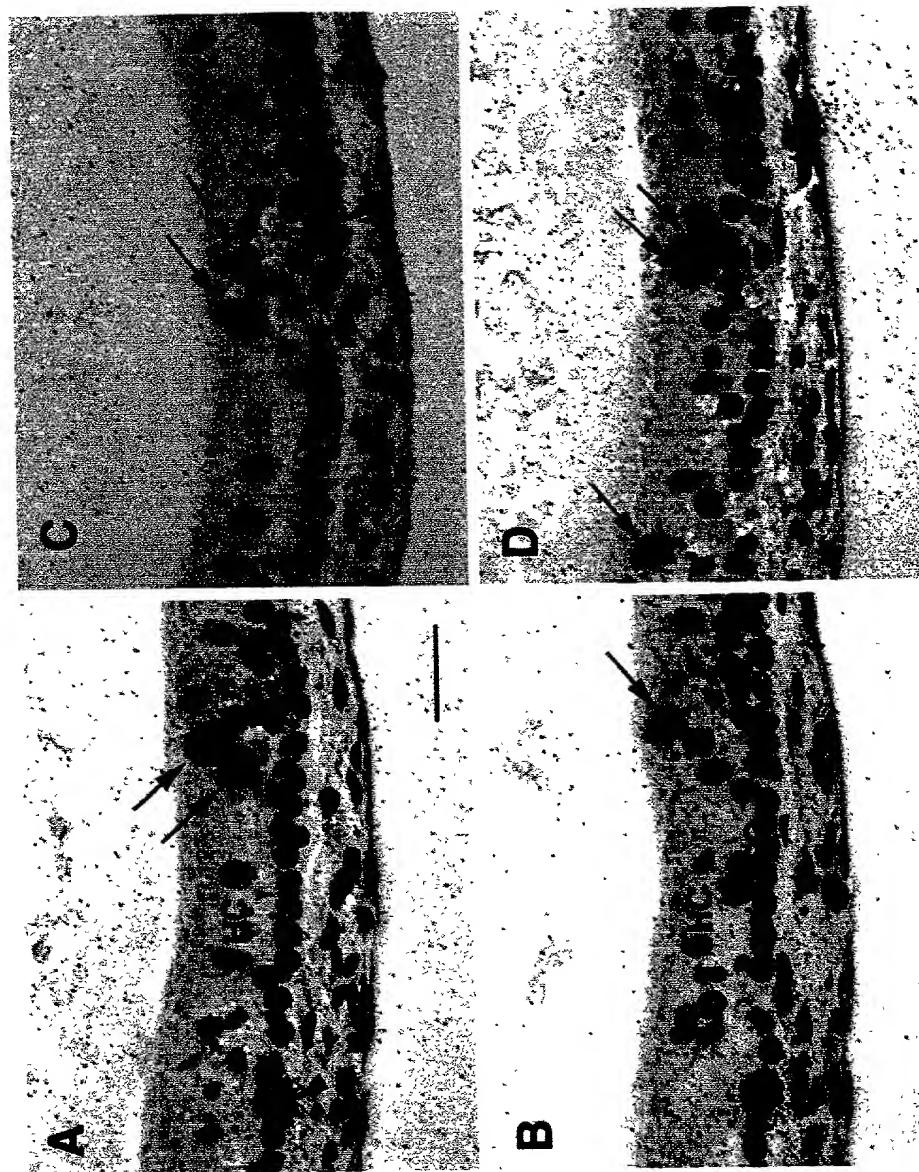


FIG. 11

Heregulin Enhances the Numbers of ^3H -thymidine Labeled Cells in Both Supporting and Hair Cell Layers

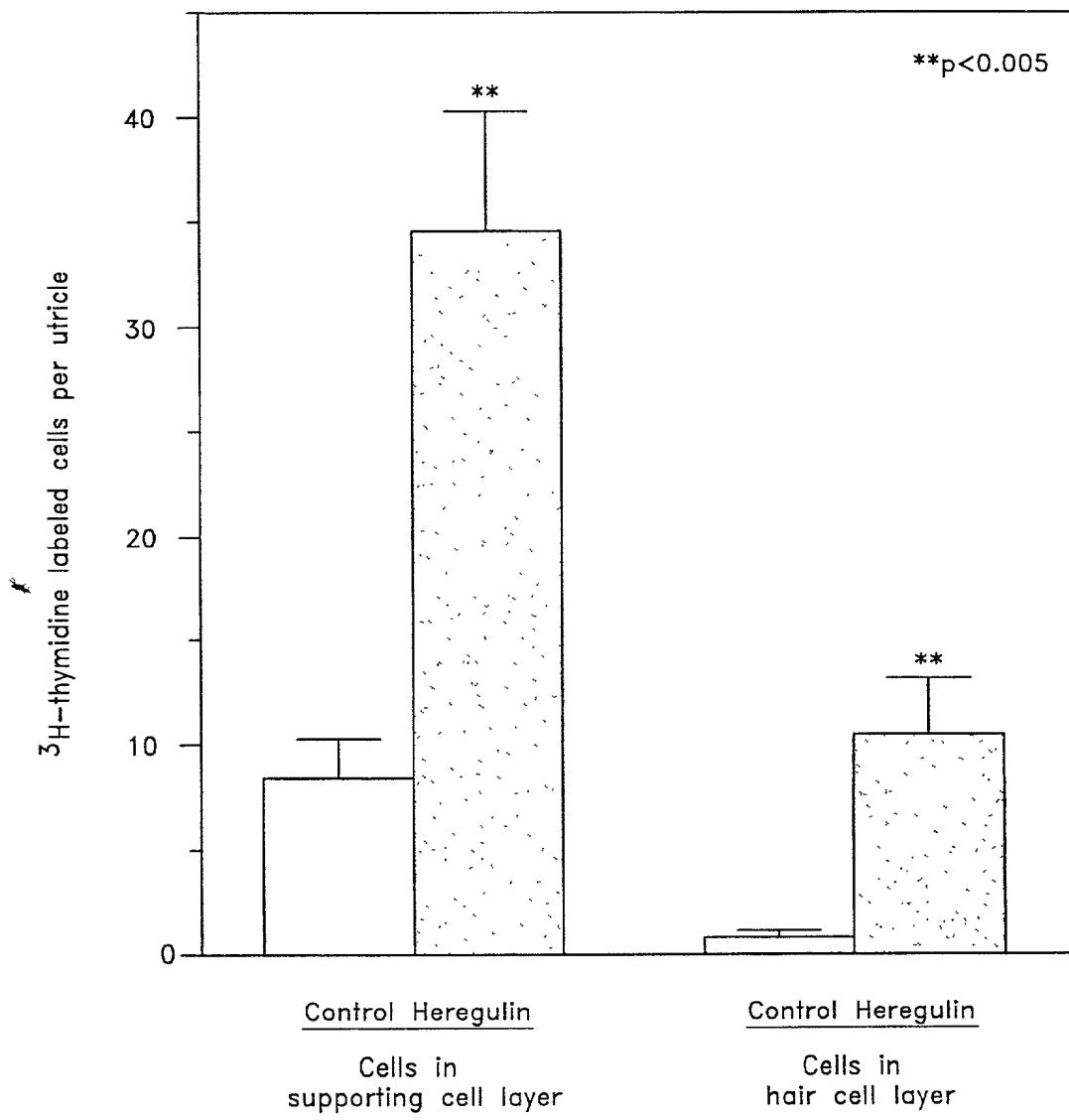


FIG. 12

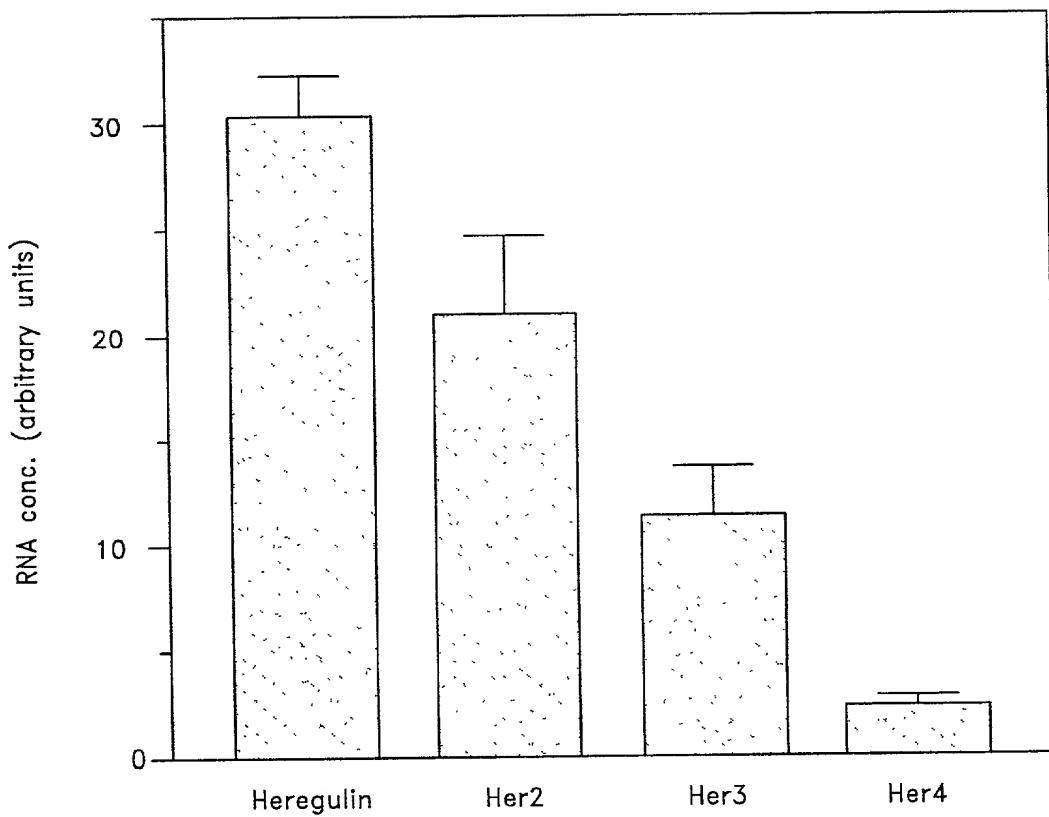


FIG. 13

HER-2 Immunostaining

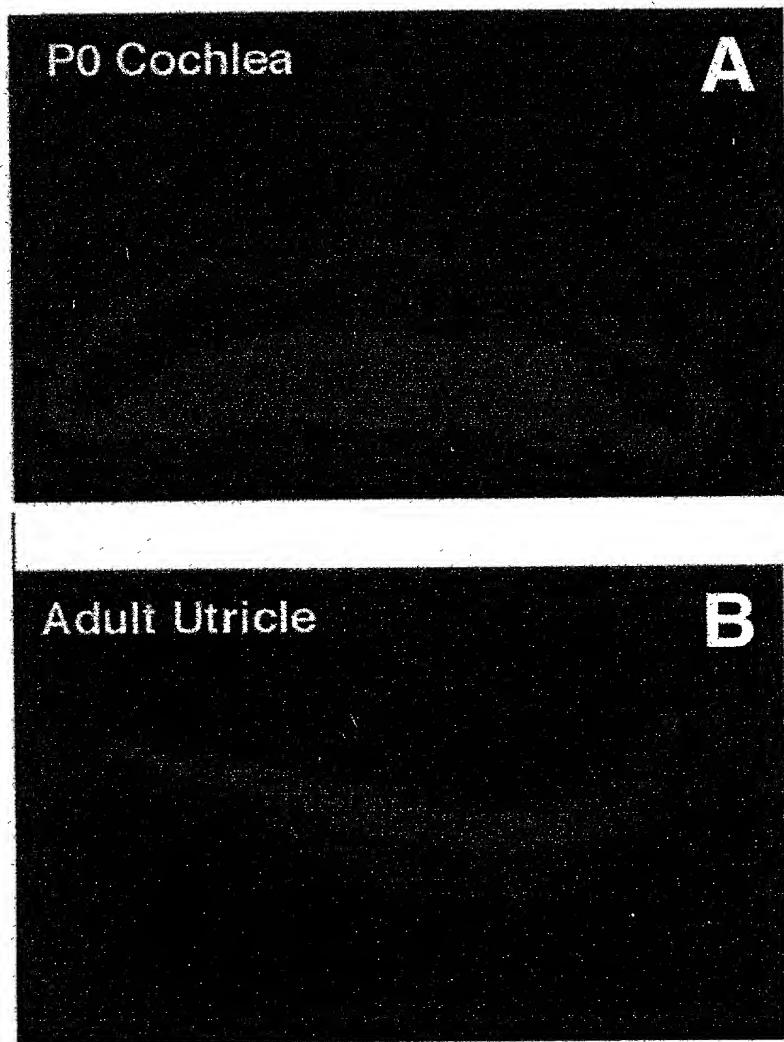


FIG.14